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FIGURE 298

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLTF
PARLPANTQILLLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLEEN
KLTELPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDALPN
LEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVP
HVALQKVVNLFKFLDLNKNPFINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLPDLRKIE
ATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHSPNPIRCDCVIRW
MNMNKTNIRFMEDSLFCVDPPEFQGNVRQVHFRDMMEICLPLIAPESFPSNLNVEAGSYVS
FHCRTAEPPQPEIYWITPSGQKLLPNTLTDFYVHSEGTLDINGVTPKEGGLYTCIATNLVGA
DLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFAVKTENSHAAQ
SARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKEYEKNNTTTLN
ACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPPLINLWEAGKEKSTS
LKVKATVIGLPTNMS

Important features:**Signal sequence:**

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708**Cell attachment sequence.**

amino acids 277-280

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FIGURE 299

GCTGTGGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTGGGAGTT
TGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCG
CCCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCAT
ACC**ATG**GGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCCTGCTGCCA
GTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCA
CAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAACAT
ACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATGAACCT
TCTTGCTTCCCATGTACAGTTTGTAATCAGATCAAAAACATAAAAGTTCCTGCACCATGACC
AGAGACACAGTGTGTCAGTGTAAGAAGGCACCTTCCGGAATGAAAACCTCCCCAGAGATGTGC
CGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAATTGTACGTCCTGGGATGAT
ATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAAACCCAGCTGCTGAAGAGACA
ATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCAGGG
ACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCCCAGCTGCT
GAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC
AGCCCGGGGACTCCTGCCTCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTA
ATTGTGCTTCTGATTGTGTTTGT**TGA**AAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTG
AAAGGTTCAGGTAGGCGCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCT
CTGCTGTGTTCCACAGACAGAAACGCCTGC

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FIGURE 300

MARIPKTLKFVVVIVAVLLPVLAISATTARQEEVPQQTVA PQQRHSFKGEECPAGSHRSEHT
GACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEMCR
KCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGT
PAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLI
VLLIVFV

Important features:**Signal peptide:**

Amino acids 1-29

Transmembrane domain:

Amino acids 240-259

N-glycosylation site:

Amino acids 77-81;140-144;156-160

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 126-130

N-myristoylation sites:

Amino acids 56-62;72-78;114-120;154-160;233-239

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FIGURE 301

CACAAGCATCTTAATTTGAATCCACAAAGTTTCATGTAATGAAAAGAAATACATAATTTTAAT
TCAACCCGAGTGTTTTCCAAGAAGATTGTATTTGCTTAAATTGCTACAGTAATTCAGAGACA
GCCCTGTCTGGACACAGAGTTACTGTGGATTTTAAAGAGACTCAGTTAAAGAATTTAGGAATT
TCTGATTCATTTAAAGGATTTACAAATTCATCAACCCCTGAAACTAAAGCAAATTGAACAGG
AAAAAAAAAAGAAGATGGGTTTTTTAAGTCCAATATATGTTATTTTCTTCTTTTTTGGAGTC
AAAGTACATTGCCAATATGAACTTATCAGTGGGATGAAGACTATGACCAAGAGCCAGATGAT
GATTACCAAACAGGATTCCCATTTTCGTCAAAATGTAGACTACGGAGTTCCTTTTTCATCAGTAT
ACTTTAGGCTGTGTCAGTGAATGCTTCTGTCCAATACTTTCCATCATCAATGTACTGTGAT
AATCGCAAACCTCAAGACTATCCCAAATATTCCGATGCACATTCAGCAACTCTACCTTCAGTTC
AATGAAATTGAGGCTGTGACTGCAAATTCATTCATCAATGCAACTCATCTTAAAGAAATTAAC
CTCAGCCACAACAAAATTAATCTCAAAAGATTGATTATGGTGTGTTTGCTAAGCTTCCAAAT
CTACTACAACCTTCATCTAGAGCATAATAATTTAGAAGAATTTCCATTTCTCTTCTTAAATCT
CTGGAAAGACTCCTTCTTGGTTACAATGAAATCTCCAAACTGCAGACAAATGCTATGGATGGG
CTAGTAAACTTGACCATGCTTGATCTCTGTTATAATTATCTTCATGATTCTCTGCTAAAAGAC
AAAATCTTTGCCAAAATGGAAAACTAATGCAGCTCAACCTCTGCAGTAACAGATTAGAATCA
ATGCCTCCTGGTTTGCCTTCTTCACTTATGTATCTGTCTTTAGAAAATAATTCAATTTCTTCT
ATACCCGAAAAATACTTCGACAACTTCCAAAACCTTCATACTCTAAGAATGTCACACAACAAA
CTACAAGACATCCCATATAATATTTTAAATCTTCCCAACATTGTAGAACTCAGTGTTGGACAC
AACAAATTGAAGCAAGCATTCTATATTCCAAGAAATTTGGAACACCTATACCTACAAAATAAT
GAAATAGAAAAGATGAATCTTACAGTGATGTGTCCTTCTATTGACCCACTACATTACCACCAT
TTAACATACATTCGTGTGGACCAAATAAACTAAAAGAACCAATAAGCTCATACATCTTCTTC
TGCTTCCCTCATATACACACTATTTATTATGGTGAACAACGAAGCACTAATGGTCAAACAATA
CAACTAAAGACACAAGTTTTTCAGGAGATTTCCAGATGATGATGATGAAAGTGAAGATCACGAT
GATCCTGACAATGCTCATGAGAGCCCAGAACAAGAAGGAGCAGAAGGGCACTTTGACCTTCAT
TATTATGAAAATCAAGAATAGCAAGAACTATATAGGTATACACTTACGACTTCACAAAACCTA
TACTTAATATAGTAAATCTAAGTAAACATGTATTACTCAAAGTAATATATTTAGAATTATGTA
TTAGTATAAGATCAGAATTGAATTTAAGTTGTTGGTGACATCTGCATCATTTTCATAGGATTAG
AACTTACTCAAAATAATGTAAATCTTTAAAAATATAAATTAGAATGACAAGTGGGAATCATAA
ATTAAACGTTAATGGTTTCTTATGCTCTTTTTAAATATAGAAATATCATGTAAAGAAAAAA
AAAAAA

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FIGURE 302

MGFLSPIYVIFFFFGVKVHCQYETYQWDEDYDQEPDDDDYQTGFPPFRQNVVDYGVPFHQYTLGCV
SECFCPTNFPSSMYCDNRKLKTIPNIPMHIQQLYLQFNEIEAVTANSFINATHLKEINLSHNK
IKSQKIDYGVFAKLPNLLQLHLEHNNLEEFPPFLPKSLERLLLGYNEISKLQTNAMDGLVNLT
MLDLCYNYLHDSLLKDKIFAKMEKLMQLNLCSNRLESMPFGLPSSLMYLSLENNSSISSIPEKY
FDKLPKLHTLRMSHNKLQDIFYNIFNLPNIVELSVGHNKLKQAFYIPRNLEHLYLQNNIEKM
NLTVMCPSIDPLHYHHLTYIRVDQNMKLKEPISSYIFFCFPHIHTIYYGEQRSTNGQTIQLKTQ
VFRFRPDDDDDESEDHDDPDNAHESPEQEGAEGHFDLHYENQE

Important features:**N-glycosylation sites:**

Amino acids 113-117;121-125; 187-191;242-246;316-320

Tyrosine kinase phosphorylation sites:

Amino acids 268-275;300-307

N-myristoylation site:

Amino acids 230-236

Leucine zipper patterns:

Amino acids 146-168;217-239

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FIGURE 303

CCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAGC
TGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTACCA
CGCTTGTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCTGGT
AGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTGTTCCTTATGAT
ACTGTGCTTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGGGGTTT
AAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGAAACAGT
CTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTTAAGGACCTCCA
TCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCATGCCTTCAA
AGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAGTGTGCACAA
AAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGCACTGCGACTG
TACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCACAACGTGATCTG
TAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGCCAACGACGCTGA
CCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCATGTTTGGCTGGTT
CACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAGGATGCCCGGAGACA
CCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGAACCTGATGATATTAG
CACTGTGGTATTAGGTGCCAACTGACTGTCATTGAGAAAGAAAGAAAGTAGTTTGCGATTGCA
GTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAAACTTTGTATTTTCAGTTT
TTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACATAAATAATTTGAGTTTAG
GTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGTAAGCTACTATCTGAACATT
AGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTTAATTTAAAAGCAAATAAAAG
CTTAACCTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAAAAAACA

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FIGURE 304

MNLVDLWLTRSLSMCLLLQSEVLMILCFHSASMC PKGCLC SSSGGLNVTC SNANLKEI PRDLP
PETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLSDNRIQ
SVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFLNAA
NDADLCNL PKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLSRQKKADEP
DDISTVV

Important features:**Signal sequence:**

Amino acids 1-33

Transmembrane domain:

Amino acids 204-219

N-glycosylation sites:

Amino acids 47-51;94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation sites:

Amino acids 37-43;45-51;110-116

FIGURE 305

CGCCACCACCTGCGGCCACCGCCCAATGAAACGCGCTCCGSGCTCCTAGTGGTTTTTTCACACTTTGTGAATTGTTCCCT
ATACTCAAATTCGCCCAAGACACCTTTGTCTCCCAAATGCCAAATGTGAAATACGCAATGGAATTTGAAGCCTGCT
ATTCGAACATGGGATTTTTCAGGAAATGGTGTCACAATTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGT
CCTGTGGCGAAAATGCTAATTGCACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCA
GCAGTAACCAAGACAGGTTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATTTAG
ATAATGTCTGTATAGCTGCAAAATTTAATAAAAATTTTAAACAAAAATCAGATCCATAAAAAGAACCTGTGGCTTTGC
TACAAGAAGCTCTATAGAAATCTGTGCACAGACTCTTCCACCAACAGATATAAATACATATAGAAATATTAGCT
AATCATCTTCATTACTAGGTTACAGAACAACACTATTCTCAGCCAGGAGACACCCPTTCTAACTCAACTCTTACTG
AATTTGTAAAAACCGTGAATAATTTTGTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATA
GGAGAACACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCCAAAAGA
CCACAGAGTTTGATACAAATTCACGGGATATAGCTCTCAAAGTTTTCTTTTTTGATTCATATAACATGAAACATA
TTCATCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGAGAAAAGCTGCATATGATTCAAATG
GCAATGTTGCAGTTGCATTTTTATATTATAAGAGTATGGTCCTTTGCTTTTCATCATCTGACAACTCTTATTGA
AACCTCAAATTTATGATAATTTCTGAAGAGGAGGAAAGAGTCCATATCTCAGTAATTTCACTCTCAATGAGCTCAA
ACCCACCCACATATATGAACCTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATAGGA
GTCTATGTGCATTTTGGAAATTACTCACCCTGATACCATTGAATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACAT
ACTCAAATGAGACCCACACCTCATGCGCGCTGTAATCACCTGCACACATTTTGCAATTTTGATGTCTCTGGTCCPT
CCATTTGGTATTTAAAGATTTATAATATCTTTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTG
CCATATGCATTTTACCTTCTGGTTCCTTCAGTGAAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCT
GTAGCCTATTTCTTGCTGAACTTGTTTTCTTGTTGGGATCAATACAAATACTAATAAGCTCTTCTGTTCAATCA
TTGCCGGACTGCTACACTACTCTCTTTTAGCTGCTTTTGCAATGGATGTGCATTTGAAGGCATACATCTCTATCTCA
TTGTTGTGGGTGTCACTACACCAAGGGATTTTGCACAAGAATTTTATATCTTTGGCTATCTAAGCCACGGCG
TGGTATTTGGATTTTTCGGCGACCATAGGATACAGATATTATGGCACAACAAGATGTTGGCTTAGCACCGAAA
ACAACTTTATTTGGAGTTTTTAFAGGACCAGCATGCCTAATCATTTCTTGTTAATCTCTTGGCTTTTGGAGTCAITCA
TATACAAAGTTTTTCGTACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACATAAGGTCTTTGTGCAA
GAGGAGCCTCGCTCTTCTGTTCCTTCTCGGCACCACCTGGATCTTTGGGGTTCTCCATGTTGTGCACGCATCAG
TGGTTACAGCTTACCTCTTCACAGTCAGCAATGCTTTCCAGGGGATGTTCATTTTTTTATTCCTGTGTGTTTTAT
CTAGAAAGATTCAAGAAGAAATATTACAGATTGTTCAAANAATGTCCCTGTGTTTTGGATGTTTAAAGTAAACAT
AGAGAATTGGTGGATAATTTACAACCTGCACAAAAATAAAATTTCCAAGCTGTGGATGACCAATGTATAAAAAAGACT
CATCAAAATATCCCAATTAATTAACACTACAGACAAAAAGTATTTTAAATCAGTTTTTCTGTTTATGCTATAGGAACF
GTAGATAATAGGTAATAATTAATGATTCATATGATATACTATGTTTTTCTATGTGAAATAGTTCTGTCAAAAATA
GTATTGCAGATATTTGGAAAGTAAATTTGGTTTTCTCAGGAGTGATATCACTGCACCCAAGGAAAGATTTTCTTTCTA
ACACGAGAAGTATATGAATGTCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTGGCTTTGAAACT
AGTCCCCCTACCACCTCGGTAAATGAGCTCCATTTACAGAAAGTGGACATAAGAGAATGAAGGGGCAGAAATATCAA
CAGTGAAGGGGAATGATAAGATGTAATTTTGAATGAACGTGTTTTTCTGTAGACTAGCTGAGAAATTTGTTGACAT
AAAAATAAGAAATTAAGAAACACATTTTACCATTTTGTGAATTTGTTCTGAACCTAAATGTCCACTAAAAACAAT
AGACTTCTGTTTTGCTAAATCTGTTTTCTTTTTCTAATATTTAAAAAAAAGGTTTACCTCCACAAATTTGA
AAAAAAA

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FIGURE 306

MKRLPLLVVVFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNECGNLTQSCGENANC
TNTGESSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNVCIANINKTLTKIRSIKEPVALLQEVYRNS
VTDLSPTDIITYIEILAESSLLGYKNNTISAKDTLSNSTLTTEFVKTVNNFVQRDTFVVWDKLSVNHRRTLTKL
MHTVEQATLRISQSFQKTTEFDTNSTDIALKVFFDSYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAF
YYKSIGPLLSSSDNFLKPKQNYDNSEEEERVISVSMSNPPTLYELEKITFTLSHRKVTDRYRSLCAFWNY
SPDTMNGSWSSEGCETYSNETHTSRCRNHLTHFAILMSSGPSIGIKDYNILTRITQLGIIISLICLAICIFTFW
FFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSTIAGLLHYFFLAFAWMCIEGIHLYLIVVGVIYN
KGFLBKNFYIFGYLSPAVVVGPSAALGYRYYGTTKVCWLSTENNFISWFIGPACLIILVNLLAFGVIIYKVERHT
AGLKPEVSCFENIRSCARGALALLFLGTTWIFGVLVHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEY
YRLFKNVPCCFGCLR

Important features:**Signal peptide:**

Amino acids 1-19

Transmembrane domain:

Amino acids 431-450;494-515;573-594;619-636;646-664

N-glycosylation sites:Amino acids 15-19;21-25;64-68;74-78;127-131;177-181;
188-192;249-253;381-385;395-399**Glycosaminoglycan attachment site:**

Amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 360-364

Tyrosine kinase phosphorylation sites:

Amino acids 36-44;670-677

N-myristoylation sites:Amino acids 38-44;50-56;52-58;80-86;382-388;388-394;
434-440;480-486;521-527**Aspartic acid and asparagine hydroxylation site:**

Amino acids 75-87

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FIGURE 307

CCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGT
ATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGC
CCGGAGGAGCGCCTTCCCTGCCGCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGA
GGCCGGGCGCGCCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGA
AGAAGATATCCTGATTGTTTCAGAGGGGAAAAATGGCACCTTTTACACATGATTTCAGAAAAGCGCAACAGAGAAT
GCCAGCTATTCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGA
ATTCTGTCTCTTGGCTCCCTGGATAAAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGT
GCCTCACAAGGCATCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAAAACAGGATGGGTGGCAGCATTTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTTCTCCAAACACCTCAAAATGCTATCTTCTTTAAACATG
TCAACAAGCTGAGTGCCCGAGGCGGGTGCCGAAATGGAGGCTTTTGTAAATGAAAGACGCATCTGCGAGTGTCTGA
TGGGTTCCACGGACCTCACTGTGAGAAAACCCCTTTGTACCCACGATGTATGAATGGTGGACTTTGTGTGACTCC
TGGTTTCTGCATCTGCCCACCTGGATTCTATGGAGTGAACGTGTGACAAAGCAAACCTGCTCAACCACCTGCTTTAA
TGGAGGGACCTGTTTCTACCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAA
ATGCCACAACCCCTGTGAAATGGAGGTAAATGCATTTGGTAAAAGCAAATGTAAGTGTTCAAAGGTTACCAGGG
AGACCTCTGTTCAAAGCCTGTCTCGAGCCTGGCTGTGGTGACATGGAACTGCCATGAACCCAAACAAATGCCA
ATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGC
AGGCGCCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTA
CATCTGGTGAACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCATAGCCTTTGTAAACCTTTTATGTGTT
GAATGTTCAAATAATGTTTACCTTAAAGAACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGC
TGATATTTACTCTTCTTTAAGTTTTCTAAGTACGCTCTGTAGCATGATGGTATAGATTTTCTTGTTTCAGTGCT
TTGGGACAGATTTTATATTATGTCAATTGATCAGGTTAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAAT
TACAATGCATTTATGGTGTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATGGGGCAAAATGCGTAAGTCACAA
GAATTTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAAGTTTTATTGTCAGATATTTAGATGTTTGTTAC
ATTTTTAAAAATTGCTCTTAATTTTTAAACTCTCAATACAATATATTTTGACCTTACCATTATTCAGAGATTCA
GTATTAAAAAATAAATTACACTGTGGTAGTGGCATTAAACAATATAATATATTCTAAACACAATGAAATAG
GGAATATAATGTATGAACTTTTTGCATTGGCTTGAAGCAATATAATATATTGTAACAAAACACAGCTCTTACCT
AATAACATTTTATCTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAATAAATAA
AAAAAA

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FIGURE 308

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGKM
APFTHDFRKAQQORMPAIPVNIHSMNETWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLLGT
VPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGCRNG
GFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFICPPGFYGVNCDKANCSTTCFN
GGTCFYPPGKCICPPGLEGEQCEISKCPQPCRNGGKCKGKCKSKGYQGDLCSPVCEPGCG
AHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDPPESNYIW

Important features:**Signal sequence:**

Amino acids 1-28

N-glycosylation sites:

Amino acids 88-92;245-249

Tyrosine kinase phosphorylation site:

Amino acids 370-378

N-myristoylation sites:

Amino acids 184-190;185-191;189-195;315-321

ATP/GTP-binding site motif A (P-loop):

Amino acids 285-293

EGF-like domain cysteine pattern signatures:

Amino acids 198-210;230-242;262-274;294-306;326-338

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FIGURE 309

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGGG
TTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGACT
CTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATGGAG
ATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTGGCCG
TGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTTTCGATG
ACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCGAGCGGAGGGG
TTTTCTTTGAAGGCTCTGTAGCCCGATTTCAGTCCAAGACGGATTCAAGCTGAAGGGCGCTA
CAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCTAGGCTGGATCCCAAGTGATAATTCCA
TCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATAACAAGACAT
ATAGACATGGAGAGAAGCTAATCATCACTTGTTCATGAAGGATTCAAGATCCGGTACCCCGACC
TACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCCCATCTGTCAAG
GCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGCTCCAGACCTCCT
TCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAACTTGATGGGTCTGCGT
ATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTGCCTTGCTCTGGAAG
CCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGCTGCCACCCGCGGCCTT
GTGAGCGCTACAACCACGGAACGTGGTGGAGTTTTACTGCGATCCTGGCTACAGCCTCACCA
GCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTCTTATCAAGTCTACTGCA
TCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCTCCTGACCACGTGGAAGATTGTGG
CGTTCACGGCAACCAGTGTGCTGCTGGTGTGCTGCTCGTCATCCTGGCCAGGATGTTCCAGA
CCAAGTTCAGGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAGTTCAGCAGTGACCCTGACT
TTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCCTATGACGAAGCTGTGAGTGGCGGCT
TGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAGGGCTGCCCCCTTACCCGTGGACG
ACCAGAGCCCCCAGCATAACCCCGGCTCAGGGGACACGGACACAGGCCAGGGGAGTCAGAAA
CCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAAGTCTGTATTACCTCCCAGGTGCC
AAGAGAGCACCCACCTGCTTCGGACAACCTGACATAATTGCCAGCACGGCAGAGGAGGTGG
CATCCACCAGCCCAGGCATCCATCATGCCCACTGGGTGTTGTTCCCTAAGAAACTGATTGATTA
AAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAAATACATGTTGATCTGTGGAGTTGATTC
CTTTCCTTCTCTTGGTTTTAGACAAATGTAAACAAAGCTCTGATCCTTAAATTTGCTATGCTG
ATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTCCTGTTTCTTCTTGACACAGACTGATTAAA
AATTAAAAGNAAAAAA

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FIGURE 310

MYHGMNPSNGDGFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGIP
ENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRIPQ
IEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLASSNG
YVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLPPMVS
HGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQTWPSTH
ETLLTTWKIVAFTATSVLLVLLLVLARMFQTKFKAHFPPRGPPRSSSSDPDFVVVDGVPVML
PSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDGPGESETCDSVSGSSEL
LQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFRLN

Important features:**Signal sequence:**

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472**N-myristoylation site.**amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

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FIGURE 311

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGAG
CGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCTGG
AGGCCGCCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGCGAGGCCCCAGCTCAGGCT
CGTGCCCACCCACCAAGTTCCAGTGCCGCACCAAGTGGCTTATGCGTGCCCCCTCACCTGGCGCT
GCGACAGGGACTTGGAAGTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCCATGTA
CCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCTGCACCGGCGTCAGTGACT
GCTCTGGGGGAAGTGCACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCAGGCGAGC
TCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCACCCAGACT
GTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAGGGGATGCCA
CAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCCACAACCATGG
GGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTCCTCTGCCGGAG
ACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGCTCAGTGCAAGCC
TGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGCCTCCGCCCCACTGG
GGTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGACCTCGCTGCCCTGAG
GACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACAGGAGGAGAGCAGTGA
TGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTTCTGGCCACGTGGAACC
TCGAACCCGAGCTCCTGCAGAAAGTGGCCCTGGAGATTGAGGGTCCCTGGACACTCCCTATGGA
GATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAGGGGCTGGCCCCAGGCAGC
TCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTGCCCCGTCTGAGGGTGGCGA
TTAAAGTTGCTTC

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FIGURE 312

MSGGWMAQVGAWRTGALGLALLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFCQRT
SGLCVPLTWRCDRDLDCSDGSDEEEECRIEPCQTQKGQCPPPPGLPCPCTGVSDCSGGTDKKLRN
CSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVTLES
VTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLLLLSW
LRAQERLRPLGLLVAMKESLLLSEQKTSPL

Important features:**Signal sequence:**

Amino acids 1-30

Transmembrane domain:

Amino acids 231-248

N-glycosylation sites:

Amino acids 126-130;195-199;213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation sites:Amino acids 3-9;10-16;26-32;30-36;112-118;166-172;212-218;
224-230;230-236;263-269**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 44-55

Leucine zipper pattern:

Amino acids 17-39

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FIGURE 313

CGGACGCGTGGGCGTCCGGCGGTCCGAGAGCCAGGAGGCGGAGGCGCGGGCCAGCCTGGGCCCCAGCCCACAC
CTTCAACCAGGGCCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTACTGCTGTTGCTGCCGCTGGCTGGCCAC
TTGGCTCTGGGTGCCAGCAGGGTCCGTGGGCGCCGGGAGCTAGCACCGGGTCTGCACCTGCCGGGCATCCGGGAC
GCGGGAGGCCGGTACTGCCAGGAGCAGGACCTGTGCTGCCGCGGGCCGTGCCGACGACTGTGCCCTGCCCTACCTG
GGCGCCATCTGTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTCTGC
CTCGGCGTGCCACCCCCCTTTTCCCCCGATCCAAGGATSTATGCATGGAGGTCTGATCTATCCAGTCTTGGGAACG
TACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGTGGCATGGTGGATCCAGACATGATCAAAGC
CATCAACCAGGGCAACTATGGCTGGCAGGCTGGGAACCACAGCGCCTTCTGGGGCATGACCCTGGATGAGGGCAT
TCGCTACCGCCTGGGCACCATCCGCCCATCTTCCCTCGGTCTGAACATGCATGAAATTTATACAGTGTGAAACC
AGGGGAGGTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGACCAAGG
CAACTGTGCAGGCTTCCTGGGCGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCTCAATCCATTCTCTGGGACA
CATGACGCCTGTCTGTGCGCCCCAGAACCTGCTGTCTTGTGACACCCACCAGCAGCAGGGCTGCCGCGGTGGGCG
TCTCGATGGTGCTGCTGGTTCCTGCGTCCCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCGGTGA
ACGAGACGAGGCTGGCCCTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGGCAAGCGCCAGGCCAC
TGCCCACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTCCAA
CGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGGTGCATGAGGACTTCTT
CCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAAGCCTTGGGAGGCCAGAGAGATACCGCCGGCATGGGAC
CCACTCAGTCAAGATCACAGGATGGGGAGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGC
CAACTCCTGGGGCCCAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCGACATCGA
GAGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCACTGAGGCTGCGGGCACCACGC
GGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGCGGGAAGAGGCCCAATGGGGCGGTGACCCACAGCCTCGCCCCA
CAGAGCCCCGGGGCGAGGCGGGCGCCAGGGCGCTAATCCCGGCGGGGTTCGCTGACGCAGCGCCCCCGCTGGG
AGCCGCGGGCAGGCGAGACTGGCGGAGCCCCCAGACCTCCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAG
CACAGCTGCAGATCCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGCCC
CAATACCCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTGTAGACAGGGTCTTGCTCCGTGGCCAGGTGGAG
TGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTCAAGTGACCCTCCACCTCAGCCTCTCAAG
TAGCTGGGACTACAGGTGCACCACCACACCTGGCTAATTTTTGTATTTTTTGTAAAGAGGGGGGTCTCACTGTGT
TGCCAGGCTGGTTTCGAACCTCCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCCAAAGTGCTGGGATTGCAGG
CATGAGCCACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAATAAAA
CCAAAGTATTGATAAAAAAAA

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FIGURE 314

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDCA
LPYLGAICYCDLFCNRTVSDCCPDEFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNRCT
CQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

Important features:**N-glycosylation site.**

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

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FIGURE 315

CGGACGCGTGGGCCCCCTGGTGGGCCCAGCAAGATGGATCTACTGTGGATCCTGCCCTCCCTGT
GGCTTCTCCTGCTTGGGGGGCCTGCCTGCCTGAAGACCCAGGAACACCCCAGCTGCCCAGGAC
CCAGGGAACTGGAAGCCAGCAAAGTTGTCTCCTGCCAGTTGTCCCGGAGCTCCAGGAAGTC
CTGGGGAGAAGGGAGCCCCAGGTCCTCAAGGGCCACCTGGACCACCAGGCAAGATGGGCCCCA
AGGGTGAGCCAGGCCCCAGAACTGCCGGGAGCTGTTGAGCCAGGGCGCCACCTTGAGCGGCT
GGTACCATCTGTGCCTACCTGAGGGCAGGGCCCTCCCAGTCTTTTGTGACATGGACACCGAGG
GGGGCGGCTGGCTGGTGTTCAGAGGCGCCAGGATGGTTCTGTGGATTTCTTCCGCTCTTGGT
CCTCCTACAGAGCAGGTTTTTGGGAACCAAGAGTCTGAATTCTGGCTGGGAAATGAGAATTTGC
ACCAGCTTACTCTCCAGGGTAACTGGGAGCTGCGGGTAGAGCTGGAAGACTTTAATGGTAACC
GTACTTTCGCCCCTATGCGACCTTCCGCCTCCTCGGTGAGGTAGACCACTACCAGCTGGCAC
TGGGCAAGTTCTCAGAGGGCACTGCAGGGGATTCCTGAGCCTCCACAGTGGGAGGCCCTTTA
CCACCTATGACGCTGACCACGATTCAAGCAACAGCAACTGTGCAGTGATTGTCCACGGTGCCT
GGTGGTATGCATCCTGTTACCGATCAAATCTCAATGGTCGCTATGCAGTGTCTGAGGCTGCCG
CCCACAAATATGGCATTTGACTGGGCCTCAGGCCGTGGTGTGGGCCACCCCTACCGCAGGGTTC
GGATGATGCTTCGATTAGGGCACTCTGGCAGCCAGTGGCCCTTATCTCTCCTGTACAGCTTCGG
ATCGTCAGCCACCTTGCCTTTGCCAACCACCTCTGCTTGCTGTCCACATTTAAAAATAAAAT
CATTTTAGCCCTTTCA

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FIGURE 316

MDLLWILPSLWLLLLGGPACLKTQEHPSCPGPRELEASKVVLLPSCPGAPGSPGEKGAPGPQG
PPGPPGKMGPKEPGPRNCRELLSQGATLSGWYHLCLPEGRALPVFCMDTEGGGWLVFQRRQ
DGSVDFFRSWSSYRAGFGNQESEFWLGNENLHQLTLQGNWELRVELEDENGRTFAHYATFRL
LGEVDHYQLALGKFSEGTAGDSLHSGRPFTTYDADHDSSNSNCAVIVHGAWWYASCYRSNL
NGRYAVSEAAAHKYGIDWASGRGVGHPYRRVRMMLR

Important features:**Signal peptide:**

Amino acids 1-16

N-glycosylation site:

Amino acids 178-182

Glycosaminoglycan attachment site:

Amino acids 272-276

Tyrosine kinase phosphorylation site:

Amino acids 188-197

N-myristoylation sites:

Amino acids 16-22;89-95;144-150;267-273

Fibrinogen beta and gamma chains C-terminal domain signature:

Amino acids.242-255

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FIGURE 317

CCCAAGCCAGCCGAGCCGCCAGAGCCGCGGGCCGCGGGGGTGTGCGGGGCCCCAACCCAGG**AT**
GCTCCCCCTGCGCCTCCTGCCTACCCGGGTCTCTACTGCTCTGGGCGCTGCTACTGTTGCTCTT
GGGATCAGCTTCTCCTCAGGATTCTGAAGAGCCCGACAGCTACACGGAATGCACAGATGGCTA
TGAGTGGGACCCAGACAGCCAGCACTGCCGGGATGTCAACGAGTGTCTGACCATCCCTGAGGC
CTGCAAGGGGGAAATGAAGTGCATCAACCACTACGGGGGGCTACTTGTGCCTGCCCCGCTCCGC
TGCCGTCATCAACGACCTACATGGCGAGGGACCCCCGCCACCAGTGCCTCCCGCTCAACACCC
CAACCCCTGCCCACCAGGCTATGAGCCCGACGATCAGGACAGCTGTGTGGATGTGGACGAGTG
TGCCAGGGCCCTGCACGACTGTGCCCCAGCCAGGACTGCCATAACTTGCCTGGCTCCTATCA
GTGCACCTGCCCTGATGGTTACCGCAAGATCGGGCCCCGAGTGTGTGGACATAGACGAGTGCCG
CTACCGCTACTGCCAGCACCGCTGCGTGAACCTGCCTGGCTCCTTCCGCTGCCAGTGCGAGCC
GGGCTTCCAGCTGGGGCCTAACAACCGCTCCTGTGTTGATGTGAACGAGTGTGACATGGGGGC
CCCATGCGAGCAGCGCTGCTTCAACTCCTATGGGACCTTCCTGTGTCGCTGCCACCAGGGCTA
TGAGCTGCATCGGGATGGCTTCTCCTGCAGTGATATTGATGAGTGTAGCTACTCCAGCTACCT
CTGTCAGTACCGCTGCGTCAACGAGCCAGGCCGTTTCTCCTGCCACTGCCCCACAGGGTTACCA
GCTGCTGGCCACACGCCTCTGCCAAGACATTGATGAGTGTGAGTCTGGTGCGCACCAGTGCTC
CGAGGCCCAAACCTGTGTCAACTTCCATGGGGGCTACCGCTGCGTGGACACCAACCGCTGCGT
GGAGCCCTACATCCAGGTCTCTGAGAACCGCTGTCTCTGCCCGGCCTCCAACCTCTATGTCG
AGAGCAGCCTTCATCCATTGTGCACCGCTACATGACCATCACCTCGGAGCGGAGCGTGCCCGC
TGACGTGTTCCAGATCCAGGCGACCTCCGTCTACCCCGGTGCCTACAATGCCTTTCAGATCCG
TGCTGGAAACTCGCAGGGGGGACTTTTACATTAGGCAAATCAACAACGTGAGCGCCATGCTGGT
CCTCGCCCGGCCGGTGACGGGGCCCCGGGAGTACGTGCTGGACCTGGAGATGGTCACCATGAA
TTCCCTCATGAGCTACCGGGCCAGCTCTGTACTGAGGCTCACCGTCTTTGTAGGGGCCCTACAC
CTTCT**G**AGGAGCAGGAGGGAGCCACCTCCCTGCAGCTACCCTAGCTGAGGAGCCTGTTGTGA
GGGGCAGAATGAGAAAGGCAATAAAGGGAGAAAGAAAGTCCTGGTGGCTGAGGTGGGCGGGTC
ACACTGCAGGAAGCCTCAGGCTGGGGCAGGGTGGCACTTGGGGGGGCAGGCCAAGTTCACCTA
AATGGGGGTCTCTATATGTTCAAGCCCAGGGGGCCCCATTGACAGGAGCTGGGAGCTCTGCAC
CACGAGCTTCAGTCACCCCGAGAGGAGAGGAGGTAACGAGGAGGGCGGACTCCAGGCCCGGC
CCAGAGATTTGGACTTGGCTGGCTTGCAGGGGTCCCTAAGAACTCCACTCTGGACAGCGCCAG
GAGGCCCTGGGTTCCATTCTTAACCTCTGCCTCAAACCTGTACATTTGGATAAGCCCTAGTAGTT
CCCTGGGCCTGTTTTTCTATAAAACGAGGCAACTGGAAAAAAAAAAAAA

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FIGURE 318

MLPCASCLPGSLLLWALLLLLLLGSASPQDSEEPDSYTECTDGYEWDPDSQHCRDVNECLTPE
ACKGEMKCINHYGGYLCLPRSAAVINDLHGEGPPPPVPPAQHPNFCPPGYEPDDQDSCVDVDE
CAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCE
PGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDECYSSY
LCQYRCVNEPGRFSCHCPQGYQLLATRLCQDIDECESGAHQCEAQTVCNFGGYRCVDTNRC
VEFYIQVSENRCCLCPASNPLCREQPSSIVHRYMTITSERVSPADVFIQATSVYPGAYNAFQI
RAGNSQGDFYIRQINNVSAMLVLARFVTGPREYVLDLEMVTMNSLMSYRASSVLRLTVFVGAYTF

Important features:**Signal sequence:**

Amino acids 1-25

N-glycosylation sites:

Amino acids 198-202;394-398

N-myristoylation sites:Amino acids 76-82;145-151;182-188;222-228;290-296;305-311;
371-377;381-387**Aspartic acid and asparagine hydroxylation sites:**

amino acids 140-152;177-189;217-229;258-270

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FIGURE 319

GCTGGGGACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCCTCTGCCTCCTC
TCAAAGGTGCGTACCCAGCTGTGCCCGACACCATGTACCTGCCCCCTGGCCACCTCCCCGATGC
CCGCTGGGAGTACCCCTGGTGTGCTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGGCGGCTG
GGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGGTCTGCCAGCCCCGGG
GCAGGACCCGGTGGCCGGGGGGCCCTGTGCCTCTTGGCAGAGGACGACAGCAGCTGTGAGGTG
AACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGCATCCGCTGCCGCTGC
GAGGACGGCGGCTTCACCTGCGTGCCGCTGTGCAGCGAGGATGTGCGGCTGCCCAGCTGGGAC
TGCCCCCACCACAGGAGGGTCGAGGTCCTGGGCAAGTGCTGCCCTGAGTGGGTGTGCGGCCAA
GGAGGGGGACTGGGGACCCAGCCCCCTTCCAGCCCAAGGACCCACAGTTTTCTGGCCTTGTCTCT
TCCCTGCCCCCTGGTGTCCCTGCCCAGAATGGAGCACGGCCTGGGGACCCCTGCTCGACCACC
TGTGGGCTGGGCATGGCCACCCGGGTGTCCAACCAGAACCGCTTCTGCCGACTGGAGACCCAG
CGCCGCCTGTGCCTGTCCAGGCCCTGCCCACCCTCCAGGGGTGCGAGTCCACAAAACAGTGCC
TTCTAGAGCCGGGCTGGGAATGGGGACACGGTGTCCACCATCCCCAGCTGGTGGCCCTGTGCC
TGGGCCCTGGGCTGATGGAAGATGGTCCGTGCCCAGGCCCTTGGCTGCAGGCAACACTTTAGC
TTGGGTCCACCATGCAGAACACCAATATTAACACGCTGCCTGGTCTGTCTGGATCCCGAGGTA
TGGCAGAGGTGCAAGACCTAGTCCCCTTTCCTCTAACTCACTGCCTAGGAGGCTGGCCAAGGT
GTCCAGGGTCCTCTAGCCCACCTCCCTGCCTACACACACAGCCTATATCAAACATGCACACGGG
CGAGCTTTCCTCTCCGACTTCCCCTGGGCAAGAGATGGGACAAGCAGTCCCTTAATATTGAGGC
TGCAGCAGGTGCTGGGCTGGACTGGCCATTTTTCTGGGGGTAGGATGAAGAGAAGGCACACAG
AGATTCTGGATCTCCTGCTGCCTTTTCTGGAGTTTGTAAAATTGTTCCCTGAATACAAGCCTAT
GCGTGA

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FIGURE 320

MRGTPKTHLLAFSLLCLLSKVRTQLCPTPCTCPWPPPRCPPLGVPLVLDGCGCCRVCCARRLGEP
CDQLHVCDASQGLVCQPGAGPGGRGALCLLAEDDSSCEVNGRLYREGETFQPHCSIRCRCEG
GFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPEWVCQGQGGGLGTQPLPAQGPQFSGLVSSLP
PGVPCPEWSTAWGPCSTTCGLGMATRVSNQNRFCRLETQRRCLLSRPCPPSRGRSPQNSAF

Important features:

Signal sequence:

Amino acids 1-23

N-myristoylation sites:

Amino acids 3-9;49-55;81-87;85-91;126-132;164-170;166-172;
167-173;183-189;209-215

Insulin-like growth factor binding proteins signature:

Amino acids 49-65

von Willebrand C1 domain:

Amino acids 107-124

Thrombospondin 1 Homology Block:

Amino acids 201-216

IGF binding protein site:

Amino acids 49-58

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FIGURE 321

[illegible]

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FIGURE 322

MMGLSLASAVLLASLLSLHLGTATRGSDISKTC CFQYSHKPLPWTWVRSYEFTSNSCSQRAVI
FTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

Important features:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine).

amino acids 23-88

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FIGURE 323

ACCGAGCCGAGCGGACCGAAGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGGGCGTGAGGAGCA
TGCCCAAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCTGGGCTCAGTGCTGTGAGGCTCGGCCA
CGGGCTGCCCCGCCCCGCTGCGAGTGCTCCGCCCAGGACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAG
TCCCCGAGGGCATCCCCACCGAGACCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACG
AGTTCGCCAGCTTCCCCCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGCGCCT
TCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCGAGCAACCGCCTGAAGCTCATCCCGCTAGGCGTCTTCA
CTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGATCGTTATCCTACTGGACTACATGTTTCAGG
ACCTGTACAACCTCAAGTCACTGGAGGTTGGCGACAATGACCTCGTCTACATCTCTACCCGCGCCTTCAGCGGCC
TCAACAGCCTGGAGCAGCTGACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACCTGC
ACGGCCTCATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGCTGTACC
GACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAACCTGCCTCTACGGCCTCAACC
TGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCCCTACCTGGCCGTCCGCCACCTAGTCTATCTCC
GCTTCTCAACCTCTCCTACAACCCCATCAGCACCATTTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGG
AGATCCAGCTGGTGGGCGGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGC
TCAATGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGGAGACACTCA
TCCTGGACTCCAACCCGCTGGCCTGCGACTGTCCGCTCCTGTGGGTGTTCCGGCGCCGCTGGCGGCTCAACTTCA
ACCGGCAGCAGCCACGCTGCGCCACGCCCCGAGTTTGTCCAGGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTAC
TGCCCAACTACTTCACTGCCCCCGCGCCCGCATCCGGGACCGCAAGGCCCAGCAGGTGTTTGTGGACGAGGGCC
ACACGGTGCAGTTTGTGTGCCGGGCGCGATGGCGACCGCGCCCGCCCATCCTCTGGCTCTCACCCCGAAAGCACC
TGGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCTACGCCCAGGTAC
AGGACAACGGCACGTACCTGTGCATCGCGCCCAACGCGGGCGGCAACGACTCCATGCCCGCCACCTGCATGTGC
GCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAAGACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAG
AGGCCAACAGCACCCGCGCCACTGTGCCTTTCCCTTCGACATCAAGACCTCATCATCGCCACCACCATGGGCT
TCATCTCTTTCTGGGCGTCTCTCTTCTGCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACACAA
AGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCGAGGCATCAGCTCCGCCGACGCGCCCCGCAAGT
TCAACATGAAGATGATA**TGA**AGGCCGGGGCGGGGGCAGGGACCCCCGGCGCGCCGGGCAGGGGAAGGGGCCTGGT
CGCCACCTGCTCACTCTCCAGTCTTCCACCTCCTCCCTACCTTCTACACAGTTCTCTTTCTCCCTCCCGCC
TCCGTCCCCTGCTGCCCCCGCCAGCCCTCACCACCTGCCCCCTTCTACCAGGACCTCAGAAGCCCAGACCTGG
GGACCCACCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCAATAAT
TCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTTCAATAAATATGGATTTTATGAAACTTGAATAA
TAAAAAGAGAAAAAACTAAAAA

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FIGURE 324

MQVSKRMLAGGVRSMPSPLLACWQPIILLVLGSSVLGSGSATGCPPRCECSAQDRAVLCHRKCFVAVPEGIPTETRL
LDLGKNRIKTLNQDEFASFFPHLEEELELNENIVSAVEPGAFNNLFNLR TLGLRSNRLKLIPLGVFTGLSNLTKQDI
SENKIVILLDYMEQDLYNLKSLEVGDN DLVYISHRAFSGLSLEQLTLEKCNLT SIPTEALSHLHGLIVLRRLRL
NINAI RDYSFKRLYRLKVLEISHWPYLD TMT PNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPIS
TIEGSM LHELLRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLT TLEESVFH SVGNLET LILDSNPLACDC
RLLWVFERRWRNLNENRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQVFVDEGHTVQFVCRADG
DPPPAI LWLSPRKHLVSAKSNGRITVFPDGTLEVRYAQVQDNGTYLCIAANAGGND SMPAHLHVRSYSPDWPHQP
NKTFAFISNQPGEGEANSTRATVPFPFDIKTLIIATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPR
KSDAGISSADA PRKFNMKMI

Important features:**Signal sequence:**

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345, 492-496,
505-509, 526-530, 542-546**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353, 607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143, 262-268, 320-326,
344-350, 359-365, 493-499, 503-509, 605-611**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

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FIGURE 325

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGAG
GCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGAGG
AGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAGGAG
GAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAACGGAG
AGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGAGTAGG
AAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGGAAAGAC
ACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTGGCTGCTT
TGGCATTGTTGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCTTGGAGGGAC
AGGGTCCCAGAAGGAGGGGGACAGAGGAGCTGAGAGAGGGGGGACAGGGCGTTGGGCAGGGGTCC
CTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCTCGAGCGCTGGTACTC
TGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGGACTGGTGGAGC
TACAAGGATAATCTCCAGGGAAACTTCGTGCCAGGGCCTCCTTTCTGGGGCCTGGTGAATGCA
GCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGAGCTGAAGAGGGTT
CTTTATGACCCCTTTCTGCCCCCATTAAGGCTCAGCACTGGAGGAGAGAAGCTCCGGGGAACC
TTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCTGTGGTCAATGTGTCT
GGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAACCTGCGGCTGCTGTTTGGAGCTCGCGAC
GGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTGAGGTGCAGCTCATTAC
TTCAACCAGGAACCTCTACGGGAATTTACAGCGCTGCCTCCCGCGGCCCCAATGGCCTGGCCATT
CTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCTTCCTCAGTCGCCTCCTTAACCGC
GACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTCTTCAAGACCTGAGCCTGGAG
CTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGCTCTCTCAGCACCCCGCCCTGC
TCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAATATCACCTCCCTTCAGATGCAC
TCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCTTCCAGAGCCTCAGCGGTAACAGC
CGGCCCCCTGCAGCCCTTGGCCCACAGGGCACTGAGGGGCAACAGGGACCCCCGGCACCCCGAG
AGGCGCTGCCGAGGCCCCAACTACCGCCTGCATGTGGATGGTGTCCCCCATGGTCGCTGAAGAC
TCCCCTTCGAGGATTGCACCCGCCCCGTCTAAGCCTCCCCACAAGGCGAGGGGAGTTACCCCT
AAAACAAAGCTATTAAAGGGACAGAATACTTA

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FIGURE 326

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCA
VGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLY
SHRLSELRLLEFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSLFVN
VASTSNPFLSRLNDRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSETVTW
ILIDRALNITSLQMHSLRLLSQNPFSQIFQSLSGNSRPLQPLAHRALRGNRDRHPERRCRGP
NYRLHVDGVPHGR

Important features:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 177-199

N-glycosylation sites:

Amino acids 118-122;170-174;260-264

Eukaryotic-type carbonic anhydrases proteins:

Amino acids 222-271;128-165;45-93

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FIGURE 327

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCAGCCAGGGTGCAGCCACACCAGGACTGTGTTGAAGGGTGTT
TTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACACAGTGTCTGAGAACATTTACATTATAGATAA
GTAGTACATGGTGGATAACTTCTACTTTTAGGAGGACTACTCTCTTCTGACAGTCTTAGACTGGTCTTCTACACT
AAGACACCATGAAGGAGTATGTGCTCCTATTATTCTGGCTTTGTGCTCTGCCAAACCCCTTCTTTAGCCCTTCAC
ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATGATG
ATGATGATGAGGACAACCTCTCTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTTCCATTTGATCTGTTTCCAA
TGTGTCCATTTGGATGTCAGTGCTATTACGAGTTGTACATTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCA
ACATTCATTTGATACTCGAATGCTTGATCTTCAAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAG
GACTCACTTCACTTTATGGTCTGATCCTGAACAACAACAAGCTAACGAAGATTACCCCAAAGCCCTTTCTAACCA
CAAAGAAGTTGCGAAGGCTGTATCTGTCCCACAATCACTAAGTGAAATACCACCTTAATCTTCCCAAATCATTAG
CAGAACTCAGAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACACG
TTTTGGAAATGAGTGCAAACCCCTCTTGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGTGTTC
ATATCAGAATTGCAGAAGCAAACTGACCTCAGTTCCFAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAG
ATTATAATAAAATTTCAACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAA
ACAACAAAATCACAGATATCGAAAATGGGACTCTTGCTAACATACCACGTGTGAGAGAAATACATTTGGAAAACA
ATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATAATCTTCCTTCATTCTAATTCAA
TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCCAAAGATGAAGAAATCTTTATACAGTGCAATAAGTT
TATTCACAACCCCGGTGAAATACTGGGAAATGCAACCTGCAACATTTCTGTTGTGTTTGGAGCAGAATGAGTGTTT
AGCTTGGGAACCTTTGGAATGTAAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACAT
TTGGAATACTTGAACCTCTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCAAGTGGTAAGTCC
ACTGACTTATTTTATGACAAGAAATTTCAACGGAAATTTTGCCAAACTATTGATACATAAGGGGTTGAGAGAAACA
AGCATCTATTGCAGTTTCTTTTTTGGGTACAAATGATCTTACATAAATCTCATGCTTGACCAATTCCTTTCTTCAT
AACAAAAAAGTAAGATATTCGGTATTTAACACTTTGTTATCAAGCACATTTTAAAAGAACTGTACTGTAAATGG
AATGCTTGACTTAGCAAAATTTGTGCTCTTTCATTTGCTGTTAGAAAAACAGAAATTAACAAAGACAGTAATGTGA
AGAGTGCATTACACTATTCTTATTCTTTAGTAACTTGGGTAGTACTGTAATATTTTAAATCATCTTAAAGTATGA
TTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGTCTTTATGTTTAAAACATAATTTCTTAAAA
TAAAGCCTTCAGTAAATGTTTATTACCAACTTGATAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATAT
GCTTTTTTTTTTTTAAATTATTACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAAC
CGCATTTTAAATGATCCGCTATTATAAGCTTTTAAATAGCATGAAAAATGTTAGGCTATATAACATTGCCACTTCAA
CTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCTTGGAAGAGCCTGGACACTAACAATCTACACC
AAATTGTCCTTCAAATACGTATGGACTGGATAACTCTGAGAAACACATCTAGTATAACTGAATAAGCAGAGCAT
CAAATTAAACAGACAGAAACCGAAAGCTCTATATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAA
CATATGTAATCAGAAAACAGGGAAATTTTCATTAAAAATATTGGTTTGAAAT

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FIGURE 328

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDEDNSLFPTREPRS
HFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDEFKGLTS
LYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDT
FKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI
STVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLNENKLLKKIPSGLPPELKYLQI
IFLHSNSIARVGVNDFCPTVPKMKKSLSAISLENNPVKYWEMQPATFRCVLSRMSVQLGNFGM

Important features:**Signal sequence.**

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

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FIGURE 329

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGCA
TCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGTGT
TTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGTGTT
CAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACCAGCG
GCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGCCTGCT
GAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCCGCTCCC
GCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACCTCAGTTTGA
TTACACAGTACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCTCAATACCA
TGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCATGCAGCAAAT
GTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTCTTTCACCAAC
CTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTGGAGTCCACCCG
TTGPTTGCTGGCTGGGCTTTTCCAGTGTCAGAAAGAAGGACCCATCATCATCCACACTGATGA
AGCAGATTGAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACCAG
AGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTGAAAAGGTGAAGGA
CAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCTGGACAACGTGGCTGC
CGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTGCACGGATGATCGAACA
GAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGGGAAAGTCTTCAGATGGC
AGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGC
CCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTT
AATGACCCTGGGGATTTTTTGACCACAAATGGCCACCGTTTGCTGTTGACCTGACCATGGAAC
TTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTATTACCACGGGAAGGAGCAGGT
GCCGAGAGGTTGCCCTGATGGGCTCTGCCCCGCTGGACATGTTCTTGAATGCCATGTCAGTTTA
TACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAAACCTCAGGTGATGGAAGTTGGAAA
TGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATTTTAAAATAAAGTGCCTTTATACAATG

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FIGURE 330

MITGVFSMRLWTFVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLRMVQVFRHGARSPLKPLPLEEQVE
WNPQLLEVPPTQTFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKNYVEDIPFL
SPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPPIIHTDEADSEVLYPNYQSCWSLRQTRGRRQTASLQ
PGISEDLLKKVKDRMGIDSSDKVDDFFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMA
VGPFLLHILESNNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESKEWVQ
LYYHGKEQVPRGCPDGLCPDMLNAMS VYTLSPKEYHALCSQTQVMEVGNEE

Important features:**Signal sequence:**

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

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FIGURE 331

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCAGTCTTGTGGCTACAACATTTTCCCTTTCCT
AACAAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCCTCTTGCTGGAGAAGAAAGGGCTGAGGGCAG
AGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTGCCCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGAT
GCAGCGGAGTGAGGTGATGGAAGTCTAAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGA
CCTGGAGAGCCTGGGGGAGGGCCTGCCCTAACAAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGATAAG
ACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCCTAATATCAAATTGACTGGCTGGGTGAACCTCAACAGCCT
TTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAATAGAGATGCTTTGTAAAATAAAATTTTAA
AAAAAGCAAGTATTTTATAGCATAAAGGCTAGAGACCAAAATAGATAACAGGATTCCCTGAACATTCCTAAGAGG
GAGAAAGTATGTTAAAAATAGAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGGACC
CTGGGTCAGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTTGCAGAA
TCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCTCCTCACCGCCGCCCCCTCTC
AGCATGGAACAGAGGCAGCCCTGGCCCCGGGGCCCTGGAGGTGGACAGCCGCTCTGTGGTCTGCTCTCAGTGGTC
TGGGTGCTGCTGGCCCCCCCCAGCAGCCGGCATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACC
TTCAACCACTTGACCGTCCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGTCTATAAGCTGACA
GGCAACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCGCCCTCATC
GTGCAGCCCTGCAGCGAAGTGCTCACCCTCACCAACAATGTCAACAAGCTGCTCATCATTGACTACTCTGAGAAC
CGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCAAGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTG
GAGCCATCCACACAAGAAGGAGCACTACCTGTCCAGTGTCACAAGACGGGCACCATGTACGGGGTGATTGTGCGC
TCTGAGGGTGAGGATGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCTGTCC
AGCCGGAAGCTGCCCCGAGACCCTGAGTCCCTCAGCCATGCTCGACTATGAGCTACACAGCGATTTTGTCTCCTCT
CTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTACGGCTTTGCTAGT
GGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCCGAGACCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTC
TTCTACACCTCACGCATCGTGCGGCTCTGCAAGGATGACCCCAAGTTCCTACTCATACGTGTCCCTGCCCTTCGGC
TGCACCCGGGGCCGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCCCAG
GCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCAAAGGGCAGAAGCAGTATCACCACCCG
CCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTTGCAGATCAAGGAGCGCCTGCAGTCCTGC
TACCAGGGCGAGGGCAACCTGGAGCTCAACTGGCTGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCC
ATCGATGATAACTTCTGTGGACTGGACATCAACCAGCCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTG
TACACCACCAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGTTTTTGTGGGG
ACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCCATTACCTCCTCAGCAAA
GAGTCCCTCTTGAAGGTAGCTATTTGGTGGAGATTTAACTATAGGCAACTTTATTTTCTTGGGGAACAAAGGTGA
AATGGGGAGGTAAGAAGGGGTAAATTTGTGACTTAGCTTCTAGCTACTTCCTCCAGCCATCAGTCATTGGGTAT
GTAAGGAATGCAAGCGTATTTCAATATTTCCCAAACCTTTAAGAAAAAACCTTAAGAAGGTACATCTGCAAAAGCAAA

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FIGURE 332

MGTLGQASLFAPPGNYFWS DHSALCF AESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWPR
ALEVDSRSVLLSVVWVLLAPPAAGMPQFSTFHSEN RDWTFNH LTVHQGTGAVYVGAINRVYK
LTGNLTIQVAHKTGP EEDNKSRY PPLIVQPCSEVLTLTNNVNKLLIIDYSENRL LACGS LYQG
VCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFITAVD GKQDYFPTL
SSRKLPRDP ESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYG FASGGFVYFLTVQPE
TPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKPGDSL AQ
AFNITSQDDVLF AIFSKGQKQYHPPDD SALCAFFIRAINLQIKERLQSCYQGE GNLELNWLL
GKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNGYSVV FVGT
KSGK LKKVRVYEFRC SNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Important features:**Signal sequence:**

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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FIGURE 333

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACTGTGCCTACACCACGCCAGG
CCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCCAGAGCCCACACCATGCCGGGCACCTACGC
TCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGGCCCTGAT
GCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCCCTGGTCCTAAGGCAGGTTTACCA
GAAAGGGCTACAGGATGTAACTGCGCAATTTCAGCTACGGCCAGACCAGCCTGGACAGGCT
TAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCG
GGATGCCCTGCGCCTCACCCTGGAGCAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTC
TGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCAT
CGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCT
GGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAA
GGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGC
AGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCG
GGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCCCGGGGTGTGTGCAA
CAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGAT
GGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGA
TCACTTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGA
TGGGGCCCGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCCTGATAGAGGA
GTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAAACCTGCTGCG
GGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTTGGAGGACAA
GTTCCCGGATGAGCAGCTGAGCAGTTCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACA
GAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACTGGACAGCCAAGTTACCAGC
CAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAGTCCTTGACAGTTGTGGCCACCTT
CCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCCTGCCAGATGTCACTGTAGCAAGC
CACAGACACCCACAAAGTTCCTGTTGTGCAGGCACAAATATTTCTGAAATAAATGTTTT
GGACATAG

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FIGURE 334

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYGQ
TSLDRLRDGLVGAFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALNDTQ
KLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGLTDF
GEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQLLKK
NGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLEDVSTY
PVLIEELLSRGWSEEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSSCHSDLS
RLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

Important features:**N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

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FIGURE 335

[illegible]

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FIGURE 336

MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEW
KKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTV
TLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSS
YTMNTKTGTLQFNTVSKLDTGEYSCEARN SVGYRRCPGKRMQVDDLNISGIIAAVVVVALVIS
VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

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FIGURE 337

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCGG
CACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGAGGGCCA
TGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTTGTTCCCTGGGGCTGAGTG
CCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGCGG
TGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGGTGTCTTCATCCC
AGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATCAGGTGT
TGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCCATGCCCT
CCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCCTACAGCTGCT
CCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAACCTTAGAACTCA
ATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCATGTGGGGGCAA
ACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCAGTGGGATCGGC
AGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCC
TCACCAACCTTTTCTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCACAAATGAGGTGGGCA
CTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAG
CTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCC
GGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCC
TGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCG
CACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTC
TCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAA
TATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
TGGTGCCTGCCAGAGTCAAGCTGGCTCTCTGGTAT**TG**ATGACCCACCACTCATTGGCTAAAG
GATTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATGGGAAAG
AGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAAACCATCTCA
GTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGC
CTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTACCAAGAGT
GAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGATCTGTACCCACCCCTAT
CTAACACCACCCCTTGGCTCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCTTG
GTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAAACTAACATGAAATATGTGTT
GTTTTCAATTGCAAATTTAAATAAAGATACATAATGTTTGTATGAAAAA